SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 207

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCTCAK 60

GGSGTNNNNN NNCCGGGTGG CGGTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCGCAGG 120

GGCCCCAGGN NGGGTGTGCG CGCGACTAGG AAGACTTCCG AGCGGTCACA ACCTCGTGGC 180

AGGCGACAGC CTATCCCCAA GGCTCGYCGG YCCGAGGGCA GGTCCTGGGC TCAGCCCGGG 240

TATCCTTGGC CCCTCTATGG CAATGAGGGC TGCGGGTGGG CGGGNTGGCT CCTGTCCCCC 300

CGCGGCTCTC GGCCCAATTG GGGCCCC 327

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1               5                  10                  15

Arg Arg Pro Xaa Xaa Xaa Xaa Xaa Pro Gly Gly Gly Gln Ile Val Gly
            20                  25                  30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Xaa Gly Val Arg Ala
        35                  40                  45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
    50                  55                  60

Ile Pro Lys Ala Xaa Arg Xaa Glu Gly Arg Ser Trp Ala Gln Pro Gly
65                  70                  75                  80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Xaa Trp
                85                  90                  95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro
            100                 105
```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GACGGCGTGA ACTATGCAAC AGGGAACTTG CCCGGTTGCT CTTTCTCTAT CTTCCTCTTG 60

GCTTTGCTGT CCTGCTTGAC GGTTCCAACK ACCGCTCACG AGGTGCGCAA CGCATCCGGG 120

GTGTATCATG TCACCAACGA CTGTTCCAAC TCGAGCATCA TCTATGAGAT GGACGGTATG 180

ATCATGCACT ACCCAGGGTG CGTGCCCTGC GTTCGGGAGG ATAACCATCT CCGCTGCTGG 240

ATGGCGCTCA CCCCCACGCT TGCGGTCAAA AAYGCTAGTG TCCCCACTRC GGCAATCCGA 300

CGTCACGTCG ACTTGCTTGT TGGGGGNNCC ACGTTCTGTT CCGCTATGTA CGTGGGRGAC 360

CTTTGCGGGT CTGTCTTCCT CGCTGGCCAG CTATTCACCT TTTCACCCCG CATGCACCAT 420

ACAACGCAGG AGTGCAACTG CTCAATC 447

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Xaa Thr Ala
20 25 30

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp Cys
35 40 45

Ser Asn Ser Ser Ile Ile Tyr Glu Met Asp Gly Met Ile Met His Tyr
50 55 60

Pro Gly Cys Val Pro Cys Val Arg Glu Asp Asn His Leu Arg Cys Trp
65 70 75 80

Met Ala Leu Thr Pro Thr Leu Ala Val Lys Xaa Ala Ser Val Pro Thr
85 90 95

Xaa Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Xaa Xaa Thr Phe
100 105 110

Cys Ser Ala Met Tyr Val Xaa Asp Leu Cys Gly Ser Val Phe Leu Ala
115 120 125

Gly Gln Leu Phe Thr Phe Ser Pro Arg Met His His Thr Thr Gln Glu
130 135 140

Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCACAG 60

GACGTCAAGN TCCCGGGTGG TGGTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCGCAGG 120

GGCCCCAGGT TGGGTGTGCG CGCGACCAGG AAGACTTCCG AGCGGTCGCA GCCTCGTGAC 180

AGGCGACAGC CTATTCCTAA GGCTCGCCAG TCCGATGGCA GNNCCTGGGC TCAGCCAGGG 240

CATCCCTGGC CCCTCTATGG CAATGAGGGC TGCGGATGGG CGGGATGGCT CCTGTCCCCC 300

CGCGGCTCTC GGCCCAGTTG GGGCCCC 327

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Xaa Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Asp Arg Arg Gln Pro
50 55 60

Ile Pro Lys Ala Arg Gln Ser Asp Gly Xaa Xaa Trp Ala Gln Pro Gly
65 70 75 80

His Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro
100 105

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GACGGCGTGA ACTATGCAAC AGGGAATTTG CCTGGTTGCT CTTTCTCTAT CTTCCTCTTA 60

GCTTTTCTGT CCTGCTTGAC GGTTCCAACT ACCGCTCATG AGGTGCGCAA CGCATCCGGG 120

GTATATCATC TCACCAATGA CTGTTCCAAC TCGAGCATCA TCTATGAGAT GAGTGGTATG 180

ATCTTGCACG CCCCAGGGTG TGTGCCCTGC GTTCGGGAGA ACAACTCTTC TCGTTGCTGG 240

ATGCCRCTCA CCCCCACGCT TGCGGTCAAA GACGCTAATG TCCCTACTGC GGCAATCCGA 300

CGCCATGTCG ACTTGCTGGT TGGGACAGCC GCGTTTCGTT CCGCTATGTA CGTGGGGGAC 360

CTCTGCGGAT CCGTCTTCCT TGTCGGCCAG CTATTCACCT TTTCACCCCG CTTGTACCAT 420

ACAACACAGG AGTGCAACTG CTCAATC 447

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15

Ile Phe Leu Leu Ala Phe Leu Ser Cys Leu Thr Val Pro Thr Thr Ala
20 25 30

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Leu Thr Asn Asp Cys
35 40 45

Ser Asn Ser Ser Ile Ile Tyr Glu Met Ser Gly Met Ile Leu His Ala
50 55 60

Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp
65 70 75 80

Met Xaa Leu Thr Pro Thr Leu Ala Val Lys Asp Ala Asn Val Pro Thr
85 90 95

Ala Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Thr Ala Ala Phe
100 105 110

Arg Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val
115 120 125

Gly Gln Leu Phe Thr Phe Ser Pro Arg Leu Tyr His Thr Thr Gln Glu
130 135 140

Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA ACACCAACCG CCGCCCACAG 60

GACGTCAAGT TCCCGGGCGG TGGCCAGATC GTTGGTGGAG TCTACGTGCT ACCGCGCAGG 120

GGCCCTAGAT TGGGTGTGCG CGCAGCGCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG 180

AGGCGCCAAC CTATTCCCAA GGAGCGCCGA CCCGAGGGCA GGT 223

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1               5                  10                  15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
            20                  25                  30

Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
        35                  40                  45

Ala Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
    50                  55                  60

Ile Pro Lys Glu Arg Arg Pro Glu Gly Arg
65                  70
```

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 957 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGCA ACACCAACCG CCGCCCACAG     60

GACGTTAAAT TCCCGGGTGG GGGGCAGATC GTGGGTGGAG TTTACTTGTT GCCGCGCAGG    120

GGCCCCAGGT TGGGTGTGCG CGCGACGAGG AAGACTTCCG AGCGGTCGCA ACCTCGCGGA    180

AGGCGACAGC CTATCCCCAA GGCTCGCCGA CCCGAGGGCA GGTCCTGGGC TCAGCCTGGG    240

TACCCATGGC CCCTCTATGC TAACGAGGGC TGCGGATGGG CGGGATGGCT CCTGTCCCCT    300

CGCGGCTCCC GTCCTAGCTG GGGCCCCAAT GACCCCCGAC GTAGATCACG CAATTTGGGT    360

AAGGTCATCG ATACCCTAAC GTGTGGCTTC GCCGATCTCA TGGGGTACAT TCCGCTCGTC    420

GGCGCCCCCC TAGGGGGCGC TTCCAGAACC CTGNCACATG GTGTCCGGGT CCTGGNAGGC    480

GGCGTGATNN NNNNNNNNNN NAACCTTCCN GGTTGCTCTT TNNCTATCTT CCTCTTGGCN    540

TTACTCTCTT GCCTCACAGT CCCCACCTCT GCCTATGAGG TGCACAGCAC AACCGATGGC    600

TACCATGTCA CTAATGACTG TTCCAACGGC AGCATCGTAT ATGAGGCAAA GGACATCATC    660

CTTCACACGC CTGGGTGNGT GCCCTGCATA CGGGAAGGCA ATATCTCCCG TTGCTGGGTA    720

CCGCTCACCC CCACGCTCGC AGCGCGGATC GCGAACGCTC CCATCGATGA GGTGCGGCGT    780

CACGTCGACC TCCTCGTGGG GGCAGCCGTG TTCTGCTCAG CCATGTACAT TGGGGACCTT    840

TGTGGGGGCG TCTTCCTCGT TGGGCAATTG TTCACCTTCA CGTCCCGGCG GCATTGGACG    900

GTGCAGGACT GTAATTGTTC CATTTACTCT GGCCACATAA CGGGCCACCG NNNNNNN       957
```

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1               5                  10                  15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
            20                  25                  30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
        35                  40                  45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
    50                  55                  60

Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly
65                  70                  75                  80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Cys Gly Trp Ala Gly Trp
                85                  90                  95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
            100                 105                 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
        115                 120                 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
    130                 135                 140

Gly Gly Ala Ser Arg Thr Leu Xaa His Gly Val Arg Val Leu Xaa Gly
145                 150                 155                 160

Gly Val Xaa Xaa Xaa Xaa Xaa Asn Leu Xaa Gly Cys Ser Xaa Xaa Ile
                165                 170                 175

Phe Leu Leu Xaa Leu Leu Ser Cys Leu Thr Val Pro Thr Ser Ala Tyr
            180                 185                 190

Glu Val His Ser Thr Thr Asp Gly Tyr His Val Thr Asn Asp Cys Ser
        195                 200                 205

Asn Gly Ser Ile Val Tyr Glu Ala Lys Asp Ile Ile Leu His Thr Pro
    210                 215                 220

Gly Xaa Val Pro Cys Ile Arg Glu Gly Asn Ile Ser Arg Cys Trp Val
225                 230                 235                 240

Pro Leu Thr Pro Thr Leu Ala Ala Arg Ile Ala Asn Ala Pro Ile Asp
                245                 250                 255

Glu Val Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Val Phe Cys
            260                 265                 270

Ser Ala Met Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu Val Gly
        275                 280                 285

Gln Leu Phe Thr Phe Thr Ser Arg Arg His Trp Thr Val Gln Asp Cys
    290                 295                 300

Asn Cys Ser Ile Tyr Ser Gly His Ile Thr Gly His Xaa Xaa Xaa
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATGAGCACAA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA ATACCAACCG CCGCCCACAG 60

GACGTCAAGT TCCCGGGCGG CGGCCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG 120

GGCCCCAGAT TGGGTGTGCG CGCGACGAGA AAGACTTCTG AACGGTCCCA GCCACGTGGA 180

AGGCGCCAGC CCATCCCTAA AGATCGGNGN GCCACTGGCA GGTCCTGGGG ACGTCCAGGA 240

TATCCCTGGC CCCTGTATGG GAACGAGGGG CTCGGCTGGG CAGGATGGCT CCTGTCCCCC 300

CGAGGCTCTC 310

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Asp Arg Xaa Ala Thr Gly Arg Ser Trp Gly Arg Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly
100 105

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACGTGCGGNT NTGCCGACCT CATGGGGTAC ATNCCCGTTG TCGGCGCCCC GGTGGGCGGG 60

GTNGCCAGGG CCCTCGCGNA TGGCGTGCGG GTCCTGGAGG ACGGGATAAA TTATGNAACA 120

GGGAACCTCC CTGGTTGCTC CTTTTCTATC TTCTNGTTGG CTCTTCTGTC TTGTGTCACC 180

GTGCCTGTCT CTGNCGTTGA GGTCAAAAAT ACCAGTCAGG CCTATATGGC AACCAACGAC 240

TGCTCCAACA ACAGCATCGT ATGGCAATTG GNGGACGCGG TGCTTCATGT TCCTGGATGT 300

GTCCCCTGCG AGAATAGCTC CGGTCGGTTC CACTGTTGGA TCCCGATCTC GCCCAACATA 360

GCCGTGAGCA AACCTGGTGC TCTCACCAAG GGACTGCGGG CACGCATTGA TGCCGTCGTG 420

ATGTCCGCCA CCCTCTGCTC TGCCCTGTAC GTGGGAGATG TGTGCGGCGC AGTGATGATA 480

GCTGCACAGG CTTTCATCGT GGCACCGAAG CGCCATTACT TCGTCCAGGA ATGCAATTGC 540

TCCATATACC CAGGCCACAT TACAGGTCAT CGCATGGCG 579

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Thr Cys Xaa Xaa Ala Asp Leu Met Gly Tyr Xaa Pro Val Val Gly Ala
1 5 10 15

Pro Val Gly Gly Xaa Ala Arg Ala Leu Ala Xaa Gly Val Arg Val Leu
20 25 30

Glu Asp Gly Ile Asn Tyr Xaa Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Xaa Leu Ala Leu Leu Ser Cys Val Thr Val Pro Val Ser
50 55 60

Xaa Val Glu Val Lys Asn Thr Ser Gln Ala Tyr Met Ala Thr Asn Asp
65 70 75 80

Cys Ser Asn Asn Ser Ile Val Trp Gln Leu Xaa Asp Ala Val Leu His
85 90 95

Val Pro Gly Cys Val Pro Cys Glu Asn Ser Ser Gly Arg Phe His Cys
100 105 110

Trp Ile Pro Ile Ser Pro Asn Ile Ala Val Ser Lys Pro Gly Ala Leu
115 120 125

Thr Lys Gly Leu Arg Ala Arg Ile Asp Ala Val Val Met Ser Ala Thr
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Val Cys Gly Ala Val Met Ile
145 150 155 160

Ala Ala Gln Ala Phe Ile Val Ala Pro Lys Arg His Tyr Phe Val Gln
165 170 175

Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 957 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGAGCACAA ATCCTAAACC TCAAAGAAAA ACTAAAAGAA ACACTAACCG TCGCCCACAG 60

GACGTTAAGT TCCCGGGCGG CGGCCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG 120

GGCCCCAGGT TGGGTGTGCG CGCGCCAAGG AAGACTTCTG AACGGTCCCA GCCACGTGGA 180

AGGCGCCAGC CCATCCCAAA AGATCGGCGC GCCACTGGCA AGTCCTGGGG ACGTCCAGGA 240

TACCCTTGGC CCCTGTACGG GAACGAGGGC CTCGGCTGGG CAGGGTGGCT CCTGTCCCCC 300

CGGGGCTCTC GCCCCTCGTG GGGCCCAAAC GACCCCCGGC ACAGGTCACG CAACTTGGGT 360

AAGGTCATCG ATACCCTCAC GTGTGGCTTT GSCGACCTCA TGGGGTACAT ACCTGTCGTC 420

GGCGCCCCTG TGGGCGGCGT TGCCAGAGCC CTCGCGCATG GCGTGCGGGT CCTGGAGGAC 480

GGGATAAATT ATGCAACAGG GAACTTGCCC GGTTGCTCCT TTTCTATCTT CTTGCTGGCT 540

CTCTTGTCTT GTATCACCGT GCCCGTGTCT GCCATACAGG TTAAGAACAA CAGCCACTTC 600

TACATGGCGA CTAATGACTG TGCCAATGAC AGCATCGTCT GGCAGCTCAG GGACGCGGTG 660

CTCCATGTTC CTGGATGTGT CCCCTGTGAG AGGTCAGGTA ATAGGACCTT CTGTTGGACA 720

GCGGTCTCGC CCAACGTGGC TGTGAGCCGA CCTGGTGCTC TCACTAGAGG TCTGCGGGCT 780

CACATTGATA CCATCGTGAT GTCCGCCACC CTCTGCTCTG CCCTATACAT AGGGGACCTA 840

TGCGGCGCTG TGATGATAGC AGCGCAAGTT GCCGTCGTCT CACCGCAATA CCATACTTTT 900

GTCCAGGAAT GCAACTGCTC CATATACCCA GGCCATATCA CAGGACATCG AATGGNN 957

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Pro Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Asp Arg Arg Ala Thr Gly Lys Ser Trp Gly Arg Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100 105 110

Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Xaa Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145 150 155 160

Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165 170 175

Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Ala Ile
180 185 190

Gln Val Lys Asn Asn Ser His Phe Tyr Met Ala Thr Asn Asp Cys Ala
195 200 205

```
Asn Asp Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro
    210                 215                 220

Gly Cys Val Pro Cys Glu Arg Ser Gly Asn Arg Thr Phe Cys Trp Thr
225                 230                 235                 240

Ala Val Ser Pro Asn Val Ala Val Ser Arg Pro Gly Ala Leu Thr Arg
                245                 250                 255

Gly Leu Arg Ala His Ile Asp Thr Ile Val Met Ser Ala Thr Leu Cys
            260                 265                 270

Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Ile Ala Ala
        275                 280                 285

Gln Val Ala Val Val Ser Pro Gln Tyr His Thr Phe Val Gln Glu Cys
    290                 295                 300

Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Xaa
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```
GACGGGGTAA ATTATGCAAC AGGGAATCTG CCTGGTTGCT CTTTCTCTAT CTTCTTGTTG     60

GCTCTTCTGT CTTGTGTCAC CGTGCCTGTC TCTGCCGTGC AGGTTAAGAA CACCAGTACC    120

ATGTACATGG CAACCAATGA CTGTTCCAAC AACAGCATCA TCTGGCAAAT GCAGGGCGCG    180

GTGCTTCATG TTCCTGGATG TGTCCCGTGT GAGTTGCAGG GCAATAAGTC CCGGTGCTGG    240

ATACCGGTCA CTCCCAACGT GGCTGTGAAC CAGCCCGGCG CCCTCACTAG GGGCTTGCGG    300

ACGCACATTG ACACCATCGT GATGGTCGCT ACGCTCTGTT CTGCACTCTA CATCGGGGAC    360

GTGTGTGGCG CGGTGATGAT AGCTGCTCAG GTTGTCATTG TCTCGCCGCA ACATCACAAC    420

TTTTCCCAGG ATTGCAATTG TTCCATC                                        447
```

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```
Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1               5                   10                  15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Val Thr Val Pro Val Ser Ala
            20                  25                  30

Val Gln Val Lys Asn Thr Ser Thr Met Tyr Met Ala Thr Asn Asp Cys
        35                  40                  45

Ser Asn Asn Ser Ile Ile Trp Gln Met Gln Gly Ala Val Leu His Val
    50                  55                  60
```

```
Pro Gly Cys Val Pro Cys Glu Leu Gln Gly Asn Lys Ser Arg Cys Trp
65                  70                  75                  80

Ile Pro Val Thr Pro Asn Val Ala Val Asn Gln Pro Gly Ala Leu Thr
                85                  90                  95

Arg Gly Leu Arg Thr His Ile Asp Thr Ile Val Met Val Ala Thr Leu
            100                 105                 110

Cys Ser Ala Leu Tyr Ile Gly Asp Val Cys Gly Ala Val Met Ile Ala
        115                 120                 125

Ala Gln Val Val Ile Val Ser Pro Gln His His Asn Phe Ser Gln Asp
    130                 135                 140

Cys Asn Cys Ser Ile
145
```

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```
ATGAGCACAA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA ACACTAACCG CCGCCCACAG     60

GACGTTAAGT TCCCGGGCGG TGGCCAGATC GTTGGCGGAG TATACTTGTT GCCGCGCAGG    120

GGCCCCCGGT TGGGTGTGCG CGCGACGAGG AAAACTTCCG AACGGTCCCA GCCACGTGGG    180

AGGCGCCAGC CCATCCCTAA AGATCGGCGC TCCACTGGCA AATCCTGGGG ACGTCCAGGA    240

TACCCTTGGC CCCTGTATGG GAACGAGGGC CTTGGTTGGG CAGGATGGCT CTTGTCCCCT    300

CGAGGCTCTC                                                           310
```

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1               5                   10                  15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Arg Ser Leu Ala
            20                  25                  30

Glu Tyr Thr Cys Ala Arg Arg Gly Lys Leu Arg Arg Ser Ser Met Gly
        35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GACGGGATAA ACTACGCAAC AGGGAATCTG CCCGGTTGCT CCTTTTCTAT CTTCTTGCTG 60

GCCTTGCTAT CCTGTCTCAC TGTGCCGGCG TCCGCTGTGC AGGTCAAGAA CACCAGCCAC 120

TCTTATATGG TGACCAATGA TTGCTCAAAC AGCAGCATTG TCTGGCAGCT TAAGGATGCT 180

GTGCTTCACG TCCCTGGATG TGTTCCATGT GAGAGGCACC AAAATCAGTC TCGCTGCTGG 240

ATACCTGTGA CACCCAATGT GGCCGTGAGC CAACCTGGCG CGCTCACCAG GGGTTTGCGG 300

ACGCACATTG ACACCATCGT TGCGTCTGCT ACCGTCTGCT CAGCTTTGTA TGTGGGCGAC 360

TTCTGCGGCG CAGTGATGTT GGTCTCTCAA TTTTTCATGA TCTCCCCTCA GCACCACATC 420

TTCGTCCAGG ATTGCAACTG CTCGATA 447

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30

Val Gln Val Lys Asn Thr Ser His Ser Tyr Met Val Thr Asn Asp Cys
35 40 45

Ser Asn Ser Ser Ile Val Trp Gln Leu Lys Asp Ala Val Leu His Val
50 55 60

Pro Gly Cys Val Pro Cys Glu Arg His Gln Asn Gln Ser Arg Cys Trp
65 70 75 80

Ile Pro Val Thr Pro Asn Val Ala Val Ser Gln Pro Gly Ala Leu Thr
85 90 95

Arg Gly Leu Arg Thr His Ile Asp Thr Ile Val Ala Ser Ala Thr Val
100 105 110

Cys Ser Ala Leu Tyr Val Gly Asp Phe Cys Gly Ala Val Met Leu Val
115 120 125

Ser Gln Phe Phe Met Ile Ser Pro Gln His His Ile Phe Val Gln Asp
130 135 140

Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GACGGGATAA ACTATGCAAC AGGGAACCTG CCTGGTTGCT CCTTTTCTAT CTTCTTACTG 60

GCCCTGCTTT CTTGCATCAC CGTGCCGGTC TCTGCCGTGC AAGTTGCGAA CCGCAGTGGT 120

TCTTACATGG TGACCAATGA TTGCTCGAAC AGCAGCATCG TTTGGCAGCT CGAGGAGGCC 180

GTCCTTCACG TCCCTGGATG TGTTCCCTGT GAGTGGAAGG ACAACACCTC CCGCTGCTGG 240

ATACCGGTCA CCCCTAACAT CGCTGTGAGC CAACCTGGCG CGCTTACCAA GGGCCTGCGG 300

ACACATATTG ACATCATTGT CGCGTCCGCC ACGTTCTGCT CTGCCTTGTA TGTGGG 356

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Ala
20 25 30

Val Gln Val Ala Asn Arg Ser Gly Ser Tyr Met Val Thr Asn Asp Cys
35 40 45

Ser Asn Ser Ser Ile Val Trp Gln Leu Glu Glu Ala Val Leu His Val
50 55 60

Pro Gly Cys Val Pro Cys Glu Trp Lys Asp Asn Thr Ser Arg Cys Trp
65 70 75 80

Ile Pro Val Thr Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Xaa Thr
85 90 95

Lys Gly Leu Arg Thr His Ile Asp Ile Ile Val Ala Ser Ala Thr Phe
100 105 110

Cys Ser Ala Leu Tyr Val
115

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCCATG 60

GACGTTAAGT TCCCGGGTGG TGGCCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG 120

GGCCCCAGGT TGGGTGTGCG CGCGACTCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG 180

AGACGCCAAC CTATCCCCAA GGCGCGTCGA TCCGAGGGAA GGTCCTGGGC ACAGCCAGGA 240

TATCCATGGC CTCTTTACGG TAATGAGGGT TGCGGGTGGG CANNATGGCT CTTGTCCCCC 300

CGCGGTTCTC 310

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Xaa Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Arg Ser Arg
115

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GACGGGATCA ATTTTGCAAC AGGGAACCTC CCCGGTTGCT CCTTTTCTAT CTTCCTCTTG 60

GCACTCCTCT CGTGCCTGAC TGTCCCCGCT TCGGCCATCA ACTATCGCAA TGTCTCGGGC 120

ATTTACTATG TCACCAATGA TTGCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC 180

ATCTTGCACC TCCCAGGTTG CGTGCCCTGC GTGAGAGAGG GGAATCAGTC ACGTTGCTGG 240

GTAGCCCTTA CCCCTACCGT CGCAGCGCCA TACATCGGCG CGCCACTTGA GTCTCTACGG 300

AGTCATGTGG ACTTGATGGT GGGGGCCGCC ACTGTTTGTT CAGCCCTTTA CATCGGGGAT 360

TTRTGTGGYG GCTTGTTCCT AGTCGGTCAG ATGTTCTCTT TCCGACCAAG GCGCCACTGG 420

ACTACTCAAG ATTGCAATTG TTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30

Ile Asn Tyr Arg Asn Val Ser Gly Ile Tyr Tyr Val Thr Asn Asp Cys
35 40 45

Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
50 55 60

Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Gln Ser Arg Cys Trp
65 70 75 80

Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu
85 90 95

Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
100 105 110

Cys Ser Ala Leu Tyr Ile Gly Asp Xaa Cys Xaa Gly Leu Phe Leu Val
115 120 125

Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Asp
130 135 140

Cys Asn Cys Ser Ile
145

(2) INFORMATICN FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GACGGGATCA ATTATGCAAC AGGGAACCTT CCCGGTTGCT CTTTTTCTAT CTTCCTCTTG 60

GCACTCCTCT CGTGCCTGAC TGTTCCCGCT TCGGCCATTA ACTACCGCAA CACCTCGGGC 120

ATCTACCACG TCACCAATGA CTGCCCGAAC TCGAGCATAG TTTATGAGGC CGACCACCAC 180

ATCTTGCACC TTCCAGGTTG CGTGCCCTGC GTGAGAACTG GGAATCAGTC ACGTTGCTGG 240

GTGGCCCTTA CTCCTACCGT CGCAGCGCCA TACATCGGCG CACCGCTTGA GTCTCTGCGG 300

AGTCATGTGG ATCTGATGGT GGGGGCTGCC ACTGTTTGCT CAGCCCTTTA CATCGGGGAT 360

TTGTGTGGCG GCTTGTTCTT GGTTGGTCAG ATGTTTTCTT TCCGACCACG ACGCCACTGG 420

ACTGCCCAGG ATTGCAATTG TTCTATC 447

(2) INFORMATICN FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15

```
Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
           20                  25                  30

Ile Asn Tyr Arg Asn Thr Ser Gly Ile Tyr His Val Thr Asn Asp Cys
       35                  40                  45

Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
    50                  55                  60

Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys Trp
65                  70                  75                  80

Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu
                85                  90                  95

Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
           100                 105                 110

Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu Val
       115                 120                 125

Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Ala Gln Asp
    130                 135                 140

Cys Asn Cys Ser Ile
145
```

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
GACGGGATTA ATTATGCAAC AGGGAATCTT CCCGGTTGCT CCTTTTCTAT CTTCCTCTTG     60

GCACTTCTCT CGTGCCTGAC TGTCCCCGCT TCGGCCATTA ACTACCACAA CACCTCGGGC    120

ATCTATCATA TCACCAACGA CTGCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC    180

ATCTTGCATC TCCCAGGTTG CGTGCCCTGC GTGAGAGTGG GGAATCAGTC GAGTTGCTGG    240

GTGGCCCTTA CCCCTACCAT CGCAGCGCCA TACATCGGCG CACCGCTTGA GTCCTTGCGG    300

AGTCATGTGG ATCTGATGGT GGGGGCGGCC ACTGTCTGTT CAGCCCTTTA CATCGGGGAT    360

TTGTGTGGCG GTGCGTTCTT GGTTGGTCAG ATGTTCTCTT TCCGACCACG GCGCCACTGG    420

ACCACCCAAG ATTGCAACTG CTCCATC                                        447
```

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1               5                   10                  15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
           20                  25                  30
```

```
Ile Asn Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp Cys
        35                  40                  45

Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
    50                  55                  60

Pro Gly Cys Val Pro Cys Val Arg Val Gly Asn Gln Ser Ser Cys Trp
65                  70                  75                  80

Val Ala Leu Thr Pro Thr Ile Ala Ala Pro Tyr Ile Gly Ala Pro Leu
                85                  90                  95

Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
            100                 105                 110

Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ala Phe Leu Val
        115                 120                 125

Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Asp
    130                 135                 140

Cys Asn Cys Ser Ile
145
```

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```
GACGGGATCA ATTATGCAAC AGGGAATATT CCCGGTTGCT CYTTTTCTAT CTTCCTTYTG     60

GCACTTCTCT CGTGTCTGAC TGTCCCCGCT TCGGCCACTA ACTATCGCAA CGTCTCGGGC    120

ATCTACCATG TCACCAATGA CTGCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC    180

ATCTTAGCAC TTCCAGGTTG CGTGCCCTGC GTGAGAGTGG GGAACCAGTC ACGCTGCTGG    240

GTGGCCCTTA CCCCTACCGT CGCAGCGCCA TACACCGCGG CGCCGCTTGA GTCCCTGCGG    300

AGTCATGTGG ATCTGATGGT GGGAGCTGCC ACTGTTTGTT CAGCCCTTTA CATCGGGGAY    360

TTGTGTGGCG GCTTGTTCTT GGTTGGTCAG ATGTTCTCTT TYCAGCCTCG GCGCCACTGG    420

ACTACCCAGG ATTGCAATTG TTCCATC                                        447
```

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```
Asp Gly Ile Asn Tyr Ala Thr Gly Asn Ile Pro Gly Cys Xaa Phe Ser
1               5                   10                  15

Ile Phe Leu Xaa Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
            20                  25                  30

Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
        35                  40                  45

Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu Ala Leu
```

```
    50                  55                  60

Pro Gly Cys Val Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys Trp
65                  70                  75                  80

Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Thr Ala Ala Pro Leu
                85                  90                  95

Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
            100                 105                 110

Cys Ser Ala Leu Tyr Ile Gly Xaa Leu Cys Gly Gly Leu Phe Leu Val
        115                 120                 125

Gly Gln Met Phe Ser Xaa Gln Pro Arg Arg His Trp Thr Thr Gln Asp
    130                 135                 140

Cys Asn Cys Ser Ile
145
```

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```
GACGGGATTA ATTATGCAAC AGGGAAYCTC CCCGGTTGCT CTTTTTCTAT CTTCCTCTTG     60

GCACTTCTCT CGTGCCTGAC TGTCCCCGCT TCGGCCACCA ACTACCGCAA TGTCTCGGGC    120

ATTTACCATC TCACCAATGA CTGCCCGAAT TCAAGCATAG TGTTTGAGGC CGACCATCAC    180

ATCTTGCACC TTCCAGGATG CGTGCCCTGC GTGAAAGAGG GAAATCATTC ACGCTGCTGG    240

GTGGCCCTTA CCCCTACCGT CGCAGCGCCA TACATCGGCG CGCCACTTGA GTCTCTACGG    300

AGTCATGTGG ATGTGATGGT GGGGGCTGCC ACTGTTTGTT CAGCCCTTTA CATCGGGGAT    360

CTGTGCGGTG GCTTGTTCCT GGTTGGTCAG ATGTTCTCTT TCCGACCACG GCGCCACTGG    420

ACTACCCAGG AATGCAATTG TTCCATC                                        447
```

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
Asp Gly Ile Asn Tyr Ala Thr Gly Xaa Leu Pro Gly Cys Ser Phe Ser
1               5                   10                  15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
            20                  25                  30

Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
        35                  40                  45

Pro Asn Ser Ser Ile Val Phe Glu Ala Asp His His Ile Leu His Leu
    50                  55                  60

Pro Gly Cys Val Pro Cys Val Lys Glu Gly Asn His Ser Arg Cys Trp
65                  70                  75                  80
```

```
Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu
                85                  90                  95

Glu Ser Leu Arg Ser His Val Asp Val Met Val Gly Ala Ala Thr Val
            100                 105                 110

Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu Val
        115                 120                 125

Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Glu
    130                 135                 140

Cys Asn Cys Ser Ile
145
```

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```
GACGGGATCA ATTATGCAAC AGGGAACCTC CCCGGTTGCT CTTTCTCTAT CTTCATCCTG     60

GCACTTCTCT CGTGCCTGAC TGTCCCGGCC TCGGCTCAGC ATTATCGGAA TGTCTCGGGC    120

ATTTACCACG TCACCAACGA CTGCCCGAAC TCCAGCATAG TGTATGAGTC CGACCATCAC    180

ATCTTACACC TACCAGGGTG TGTACCCTGT GTGAAGACTG GGAACACTTC GCGCTGCTGG    240

GTGGCCTTAA CACCTACCGT GGCCGCGCCC ATACTTTCGG CTCCACTTAT GTCCGTACGG    300

CGGCATGTGG ATCTGATGGT GGGTGCAGCT ACCCTATCGT CTGCCCTCTA CGTTGGAGAC    360

CTCTGCGGGG GTGCCTTCCT AGTGGGGCAG ATGTTCACCT TCCAGCCGCG TCGCCACTGG    420

ACTGTCCAAG ACTGCAACTG TTCCATC                                        447
```

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```
Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1               5                  10                  15

Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
            20                  25                  30

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
        35                  40                  45

Pro Asn Ser Ser Ile Val Tyr Glu Ser Asp His His Ile Leu His Leu
    50                  55                  60

Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Thr Ser Arg Cys Trp
65                  70                  75                  80

Val Ala Leu Thr Pro Thr Val Ala Ala Pro Ile Leu Ser Ala Pro Leu
                85                  90                  95
```

```
Met Ser Val Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr Leu
            100                 105                 110

Ser Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu Val
        115                 120                 125

Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Val Gln Asp
    130                 135                 140

Cys Asn Cys Ser Ile
145
```

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 957 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```
ATGAGCACAC TTCCAAAACC CCAAAGAAAA ACCAAAAGAA ATACTAACCG TCGCCCTATG     60

GACGTCAAGT TCCCGGGCGG CGGCCAGATC GTTGGTGGAG TTTACTTGTT GCCGCGCAGG    120

GGCCCTCGTT TGGGTGTGCG CGCGACGAGA AAGACCTCCG AACGGTCCCA GCCTAGAGGC    180

AGGCGCCAGC CCATACCAAA GGTACGCCAG CCGACAGGCC GTAGCTGGGG TCAACCCGGC    240

TACCCTTGGC CCCTTTATGG CAACGAGGGC TGCGGATGGG CGGGATGGCT CCTGTCCCCC    300

CGCGGGTCTC GTCCTAATTG GGGCCCCAAC GACCCCCGGC GAAGGTCCCG CAACTTGGGT    360

AAGGTCATCG ATACCCTTAC ATNCGGNCTA GCCGACCTCA TGGGGTACAT CCCTGTCCTA    420

GGAGGGCCGC TTGGCGGCGT TGCGGCTGCC CTGGCGCATG GCGTTAGGGC AATCGAGGAC    480

GGGGTCAATT ACGCAACAGG GAATCTTCCT GGTTGCTCCT TTTCTATCTT CCTCTTAGCA    540

CTGTTATCGT GCCTCACTAC ACCAGCCTCA GCAATTCAAG TCAAGAACGC CTCTGGGATC    600

TACCATCTTA CCAATGACTG CTCGAACAAC AGCATCGTTT TTGAGGCGGA GACCATGATA    660

CTGCATCTTC CAGGTTGTGT CCCATGTATC AAGGCGGGGA ATGAGTCACG ATGTTGGCTC    720

CCTGTCTCCC CCACCTTAGC CGTCCCCAAC TCATCAGTGC CAATCCACGG GTTTCGCCGA    780

CACGTAGACC TCCTCGTTGG GGCAGCGGCA TTTTGTTCGG CCATGTACAT CGGAGACCTC    840

TGTGGTAGCA TAATCTTGGT AGGGCAGCTT TTTACTTTCA GGCCTAAGTA CCATCAGGTT    900

ACCCAGGATT GTAACTGCTC TATNAACNCT GGCCACGTCA CGGGACACAG GATGGCA       957
```

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```
Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1               5                  10                  15

Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
            20                  25                  30
```

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Val Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Xaa
115 120 125

Xaa Leu Ala Asp Leu Met Gly Tyr Ile Pro Val Leu Gly Gly Pro Leu
130 135 140

Gly Gly Val Ala Ala Ala Leu Ala His Gly Val Arg Ala Ile Glu Asp
145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165 170 175

Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Ile
180 185 190

Gln Val Lys Asn Ala Ser Gly Ile Tyr His Leu Thr Asn Asp Cys Ser
195 200 205

Asn Asn Ser Ile Val Phe Glu Ala Glu Thr Met Ile Leu His Leu Pro
210 215 220

Gly Cys Val Pro Cys Ile Lys Ala Gly Asn Glu Ser Arg Cys Trp Leu
225 230 235 240

Pro Val Ser Pro Thr Leu Ala Val Pro Asn Ser Ser Val Pro Ile His
245 250 255

Gly Phe Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys
260 265 270

Ser Ala Met Tyr Ile Gly Asp Leu Cys Gly Ser Ile Ile Leu Val Gly
275 280 285

Gln Leu Phe Thr Phe Arg Pro Lys Tyr His Gln Val Thr Gln Asp Cys
290 295 300

Asn Cys Ser Xaa Asn Xaa Gly His Val Thr Gly His Arg Met Ala
305 310 315

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 957 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATGAGCACAC TTCCAAAACC CCAAAGAAAA ACCAAAAGAA ACACCATCCG CCGCCCACAG 60

GACGTCAAGT TCCCGGGTGG CGGCCAGATC GTTGGTGGAG TCTACTTGCT GCCGCGCAGG 120

GGCCCGCGCT TGGGTGTGCG CGCGACGAGA AAGACTTCTG AACGGTCCCA GCCCAGAGGT 180

AGGCGCCAAC CAATACCCAA AGTGCGCCAC CAAACGGGCC GTACCTGGGC CCAGCCCGGG 240

TACCCCTGGC CTCTTTATGG AAATGAGGGC TGTGGTTGGG CAGGCTGGCT CCTGTCCCCC 300

CGCGGCTCTC GCCCAAATTG GGGCCCAAAC GACCCCCGGC GGAGGTCCCG CAACTTGGGT 360

AAAGTCATCG ACACCCTTAC TTGCGGCTTC GCCGACCTCA TGGGGTATAT CCCTGTCGTA 420

GGCGCTCCGW TGGGAGGCGT CGCGGNGGCC TTGGCGCATG GGGTCANGGN CATCGAGGAC 480

GGNGTAAATT ACGCAACAGN GAATCTTCCC GGNNGCTCTN TCTCTATCTT NCTCTTGGCA 540

CTTCTCTCGT GCCTTACAAC ACCAGCCTCC GCGGCGCATT ATACCAACAA GTCTGGCCTG 600

TACCATCTCA CCAACGACTG CCCCAACAGC AGCATCGTTT ATGAGGCGGA GACACTGATT 660

TTGCACTTGC CTGGGTGTGT ACCTTGTGTG AAGRTGRACA ATCAATCCCG GTGCTGGGTG 720

CAGGCCTCCC CGACCCTGGC AGTGCCGAAC GCGTCTACGC CAGTCACCGG GTTCCGCAAA 780

CATGTGGACA TCATGGTGGG CGCTGCCGCG TTCTGTTCAG CTATGTATGT GGGGGACCTG 840

TGCGGGGGCC TTTTCCTCGT TGGACAGCTC TTCACGCTCA GGCCTCGGAT GCATCAGGTT 900

GTCCAGGAGT GTAACTGTTC CATCTACACA GGGCATATCA CTGGACACCG AATGGCA 957

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Ile
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Val Arg His Gln Thr Gly Arg Thr Trp Ala Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Xaa
130 135 140

Gly Gly Val Ala Xaa Ala Leu Ala His Gly Val Xaa Xaa Ile Glu Asp
145 150 155 160

Xaa Val Asn Tyr Ala Thr Xaa Asn Leu Pro Xaa Xaa Ser Xaa Ser Ile
165 170 175

Xaa Leu Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Ala
180 185 190

His Tyr Thr Asn Lys Ser Gly Leu Tyr His Leu Thr Asn Asp Cys Pro
195 200 205

Asn Ser Ser Ile Val Tyr Glu Ala Glu Thr Leu Ile Leu His Leu Pro
210 215 220

Gly Cys Val Pro Cys Val Lys Xaa Xaa Asn Gln Ser Arg Cys Trp Val

```
225                 230                 235                 240

Gln Ala Ser Pro Thr Leu Ala Val Pro Asn Ala Ser Thr Pro Val Thr
                245                 250                 255

Gly Phe Arg Lys His Val Asp Ile Met Val Gly Ala Ala Ala Phe Cys
            260                 265                 270

Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu Val Gly
        275                 280                 285

Gln Leu Phe Thr Leu Arg Pro Arg Met His Gln Val Val Gln Glu Cys
    290                 295                 300

Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met Ala
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
ATGAGCACAC TTCCTAAACC TCAAAGAAAA ACCAAACGAA ACACCAACCG TCGCCCACAG     60

GACGTCAAGT TCCCGGGTGG CGGTCAGATC GTTGGTGGAG TTTACTTGTT GCCGCGCAGG    120

GGCCCTCGTT TGGGTGTGCG CGCGACGAGG AAAACTTCTG AACGGTCCCA GCCCAGGGGT    180

AGACGCCAAC CTATACCGAA GGTGCGTCAC CAAACGGGCC GTACCTGGGC TCAACCCGGG    240

TACCCCTGGC CTCTTTATGG GAATGAGGGT TGTGGCTGGG CAGGGTGGCT CCTGTCCCCC    300

CNCGGCTCTC GCCCTAATTG GGGCCCTAAT GACCCCCGGN GGAGGTCCCG CAACCTGGGT    360

AAGGTCATCG ATACCCTTAC TTGNGGSTTC GCCGACCTCA TAGAGTACAT TCC           413
```

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```
Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1               5                   10                  15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
            20                  25                  30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
        35                  40                  45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
    50                  55                  60

Ile Pro Lys Val Arg His Gln Thr Gly Arg Thr Trp Ala Gln Pro Gly
65                  70                  75                  80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
                85                  90                  95

Leu Leu Ser Pro Xaa Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
```

```
          100                 105                 110

Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Xaa
        115                 120                 125

Xaa Phe Ala Asp Leu Ile Glu Tyr Ile
    130                 135
```

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 957 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```
ATGAGCACAC TTCCAAAACC CCAAAGAAAA ACCAAAAGAA ACACAAACCG TCGCCCAATG     60

GATGTCAAGT TCCCGGGCGG CGGTCAGATC GTTGGTGGAG TCTACTTGTT ACCGCGCAGG    120

GGCCCACGTT TGGGTGTGCG CGCGACGAGG AAGACTTCGG AACGGTCCCA GGCCAGAGGT    180

AGGCGCCAAC CAATACCCAA GGTGCGCCAG AACCAAGGCC GAACCTGGGC TCAGCCTGGG    240

TACCCCTGGC CCCTTTATGG GAACGAGGGC TGCGGCTGGG CGGGGTGGCT CTTGTCCCCC    300

CGTGGCTCTC GCCCGGACTG GGGNCCCAAC GACCCCCGGN GGAGGTCCCG CAACCTGGGT    360

AAGGTCATCG ACACCCTCAC TTGCGGCTTC GCCGACCTCA TGGAGTACAT CCCTGTCGTT    420

GGCGCCCCCC TTGGAGGCGT TGCGGCGGAA CTGGNACATG GTGTCAGGGC CATCGAGGAC    480

GGGATAAACT ATGCAACAGG GAATCTTCCT GGTTGCTCTT TCTCTATCTT CCWCTTGGCA    540

CTTCTCTCGT GCCTCACCAC GCCTGCCTCC GCACTAAACT ATGCTAACAA GTCTGGGCTG    600

TATCATCTAA CCAATGACTG CCCCAATAGC AGCATTGTGT ATGAGGCGAA TGGCATGATC    660

CTGCATCTCC CGGGTTGCGT CCCCTGCGTG AAGACCGGCA ACCTGACCAA GTGTTGGCTG    720

TCGGCCTCCC CGACATTGGC GGTGCAGAAT GCGTCGGTGT CCATCAGGGG TGTCCGCGAG    780

CACGTGGACC TCTTGGTGGG TGCTGCTGCG TTCTGCTCTG CCATGTACGT GGGCGACTTA    840

TGCGGTGGGC TCTTTCTCGT TGGGCAGTTG TTCACGTTCA GACCCAGGAT GTATGAGATC    900

GCCCAGGACT GCAACTGTTC CATCTATGCA GGCCACATCA CTGGGCACCG GATGGCG       957
```

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```
Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1               5                  10                  15

Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
            20                  25                  30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
        35                  40                  45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Ala Arg Gly Arg Arg Gln Pro
```

```
    50                  55                  60

Ile Pro Lys Val Arg Gln Asn Gln Gly Arg Thr Trp Ala Gln Pro Gly
65                  70                  75                  80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
                85                  90                  95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asp Trp Xaa Pro Asn Asp Pro
            100                 105                 110

Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
        115                 120                 125

Gly Phe Ala Asp Leu Met Glu Tyr Ile Pro Val Val Gly Ala Pro Leu
    130                 135                 140

Gly Gly Val Ala Ala Glu Leu Xaa His Gly Val Arg Ala Ile Glu Asp
145                 150                 155                 160

Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
                165                 170                 175

Phe Xaa Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Leu
            180                 185                 190

Asn Tyr Ala Asn Lys Ser Gly Leu Tyr His Leu Thr Asn Asp Cys Pro
        195                 200                 205

Asn Ser Ser Ile Val Tyr Glu Ala Asn Gly Met Ile Leu His Leu Pro
    210                 215                 220

Gly Cys Val Pro Cys Val Lys Thr Gly Asn Leu Thr Lys Cys Trp Leu
225                 230                 235                 240

Ser Ala Ser Pro Thr Leu Ala Val Gln Asn Ala Ser Val Ser Ile Arg
                245                 250                 255

Gly Val Arg Glu His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys
            260                 265                 270

Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu Val Gly
        275                 280                 285

Gln Leu Phe Thr Phe Arg Pro Arg Met Tyr Glu Ile Ala Gln Asp Cys
    290                 295                 300

Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met Ala
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```
ATGAGCACAC TTCCTAAACC ACAAAGAAAA ACCAAAAAGAA ACACCAACCC CGGCCACAGG     60

ACGTTAAGTT CCCAGGCGGC GGTCAGATCG TTGGTGGAGT TTACGTGCTA CCACGCAGGG    120

GCCCCCAGTT GGGTGTGCGT GCAGTGCGCA AGACTTCCGA GCGGTCGCAA CCTCGCAGTA    180

GGCGCCAACC CATCCCCAGG GCGCGCCGAA CCGAGGGCAG GTCCTGGGCT CAGCCCGGGT    240

ACCCTTGGCC CCTATATGGG AATGAGGGCT GCGGGTGGGC AGGGTGGCTC CTGTCCCCGC    300

GCGGCTCTC                                                            309
```

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```
Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1               5                  10                  15

Xaa Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
            20                  25                  30

Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Gln Leu Gly Val Arg Ala
        35                  40                  45

Val Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Ser Arg Arg Gln Pro
    50                  55                  60

Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln Pro Gly
65                  70                  75                  80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
                85                  90                  95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
            100                 105                 110

Arg Arg Arg
        115
```

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```
GACGGAATTA ATTTCGCAAC AGGGAATTTA CCTGGTTGCT CTTTCTCTAT CTTCCTTCTG     60

GCTTTGTTCT CATGCTTGCT TACACCCACA GCCGGGCTGG AGTACCGTAA TGCCTCCGGA    120

CTCTACATGG TAACTAACGA CTGCAGTAAC GGTAGTATCG TGTATGAGGC CGGGGATATT    180

ATCCTCCACT TACCTGGCTG TGTCCCCTGC GTACGCTCTG GCAATACATC AAGATGCTGG    240

ATCCCTGTGA GCCCYACCGT CGCCGTGAAG TCGCCCTGCG CCGCCACCGC CTCTCTCCGC    300

ACGCACGTGG ATATGATGGT GGGRGCGGCC ACCCTATGCT CAGCTCTCTA CGTAGGAGAC    360

CTTTGTGGAG CGCTATTTCT TGTYGGGCAG GGGTTCTCAT GGAGACATCG CCAGCATTGG    420

ACTGTCCAGG ACTGCAACTG TTCCATC                                        447
```

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```
Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1               5                  10                  15

Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Leu Thr Pro Thr Ala Gly
            20                  25                  30

Leu Glu Tyr Arg Asn Ala Ser Gly Leu Tyr Met Val Thr Asn Asp Cys
        35                  40                  45

Ser Asn Gly Ser Ile Val Tyr Glu Ala Gly Asp Ile Ile Leu His Leu
    50                  55                  60

Pro Gly Cys Val Pro Cys Val Arg Ser Gly Asn Thr Ser Arg Cys Trp
65                  70                  75                  80

Ile Pro Val Ser Xaa Thr Val Ala Val Lys Ser Pro Cys Ala Ala Thr
                85                  90                  95

Ala Ser Leu Arg Thr His Val Asp Met Met Val Xaa Ala Ala Thr Leu
            100                 105                 110

Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ala Leu Phe Leu Xaa
        115                 120                 125

Gly Gln Gly Phe Ser Trp Arg His Arg Gln His Trp Thr Val Gln Asp
    130                 135                 140

Cys Asn Cys Ser Ile
145
```

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```
CTCGACAGTT ACTGAGAATG ACATCCGTGT CGAGGAATCA ATATACCAAT GTTGTGACTT     60

GGCCCCCGAG GCTCGCAAGG CCATAAAGTC GCTCACCGAG CGGCTGTACA TCGGGGGCCC    120

YCTAACCAAT TCAAAAGGAC AGAACTGCGG CTACCGTCGG TGCCGCGCCA GCGGCGTGCT    180

GACTACCAGC TGCGGCAACA CCCTGACATG CTACTTGAAA GCCAGAGCGG CCTGTCGAGC    240

TGCAAAGCTC CGGGACTGCA CCATGCTCGT GTGCGGGGAT GACCTTGTCG TTATCTGTGA    300

GAGTGCGGGA GTCGAGGAAG ACGCGGCGAA CCTACGAGCT                           340
```

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```
Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln
1               5                  10                  15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
            20                  25                  30
```

Glu Arg Leu Tyr Ile Gly Gly Xaa Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Cys Glu Ser Ala Gly Val Glu Glu Asp Ala Ala Asn Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CTCGACAGTT ACTGAGAACG ACATCCGTAC CGAGGRATCA ATCTATCAAT GTTGTGACTT 60

GGCCCCYGAG GCCCGCAAGG CCATAAAGTC GCTCACCGAG CGGCTGTACG TCGGGGGCCC 120

CCTAACCAAT TCAAAGGGGC AGAACTGCGG CTATCGTCGG TGTCGCGCTA GCGGCGTGCT 180

GACCACCAGC TGCGGCAACA CCCTCACATG CTACTTGAAA GCCAGGGCGG CCTGTCGAGC 240

TGCAAAGCTC CAGGACTGCA CGATGCTCGT GTGCGGAGAC GACCTTGTCG TTATCTGTGA 300

GAGCGCGGGA GTCGAGGAGG ACGCGGCGAA CCTACGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Ser Thr Val Thr Glu Asn Asp Ile Arg Thr Glu Xaa Ser Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu Ala Xaa Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Cys Glu Ser Ala Gly Val Glu Glu Asp Ala Ala Asn Leu Arg
100 105 110

Val

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CTCGACAGTT ACTGAGAACG ACATTCGTGT CGAGGAATCA ATCTACCAGT GCTGTGACTT 60

GGCCCCCGAG GCCCGCAAGG CCATAAAGTC GCTCACCGAG CGGCTGTATA TCGGGGGTCC 120

CCTAACCAAC TCAAAAGGGC AGAACTGCGG CTACCGTCGG TGCCGCGCCA GCGGCGTGCT 180

GACTACCAGC TGCGGTAATA CCCTCACATG TTACTTGAAA GCCAGGGCGG CCTGTCGAGC 240

TGCGAAGCTC CAGGACTGCA CAATGCTCGT GTGCGGAGAC GACCTTGTCG TTATCTGTGA 300

GAGTGCRGGA GTCGAGGAGG ATGCGGCGAA CCTACGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Cys Glu Ser Xaa Gly Val Glu Glu Asp Ala Ala Asn Leu Arg
100 105 110

Val

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 652 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CGTACAGCCT CCAGGACCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG 60

TACACCGGAA TTGCCAGGAC GACCGGGTCC TTTCTTGGAT CAACCCGCTC AATGCCTGGA 120

GATTTGGGCG TGCCCCCGCA AGACTGCTAG CCGAGTAGTG TTGGGTCGCG AAAGGCCTTG 180

TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCGGGAGG TCTCGTAGAC CGTGCACCAT 240

GAGCACGAAT CCTAAACCTC AAAGAAAAAC CAAAAGAAAC ACCAACCGCC GCCCACAGGA 300

CGTCAAGTTC CCGGGCGGTG GCCAGATCGT TGGTGGAGTC TACGTGCTAC CGCGCAGGGG 360

CCCTAGATTG GGTGTGCGCG CAGCGCGGAA GACTTCGGAG CGGTCGCAAC CTCGTGGGAG 420

GCGCCAACCT ATTCCCAAGG AGCGCCGACC CGAGGGCAGG TCCTGGGCGC AGCCCGGGTA 480

CCCCTGGCCC CTCTATGGTA ACGAGGGCTG CGGGTGGGCA GGTNGGCTCC TGTCCCCTCG 540

CGGCTCCCGT CCTAGTTGGG GTCCTACTGA CCCCCGGCGT AGGTCACGCA ATTTGGGTAA 600

GGTCATCGAT ACCCTCACGT GTTGNTTCGC CGACCTCATG GGGTACATAC CG 652

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1               5                  10                  15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
            20                  25                  30

Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
        35                  40                  45

Ala Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
    50                  55                  60

Ile Pro Lys Glu Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly
65                  70                  75                  80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Xaa
                85                  90                  95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
            100                 105                 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
        115                 120                 125

Xaa Phe Ala Asp Leu Met Gly Tyr Ile Pro
    130                 135
```

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CTCAACGGTC ACTGAAGCTG ATATCCGAAC AGAGGAGTCC ATATACCAAT GCTGTGACCT 60

GCACCCCGAA GCACGTGTAG CCATCAAGTC TTTGACTGAA AGGCTGTACG TCGGGGGGCC 120

CTTGACCAAT TCAAAAGGGG AGAACTGCGG CTATCGCAGA TGCCGTGCCA GCGGCGTCTT 180

GACAACCAGC TGCGGCAACA CCCTCACCTG CTATATCAAG GCCCTAGCAG CCTGTAGAGC 240

TGCCAAGCTC CAGGACTGCA CCATGCTCGT CTGTGGCGAC GACCTGGTCG TGATCTGCGA 300

GAGTGTAGGG ACCCAGGAGG ATGCGGCGAG CCTGCGAGCC 340

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ser Thr Val Thr Glu Ala Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu His Pro Glu Ala Arg Val Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Glu Asn
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Cys Glu Ser Val Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

NTCAACAGTC ACTGAGAGTG ATATCCGTAC AGAGGAGTCC ATCTACCAAT GCTGTGATCT 60

AGACCCCGAG GCTCGCAAGG CCATAAGGTC CCTCACAGAG AGGCTTTATA TCGGGGGTCC 120

CCTGACAAAC TCAAAAGGGC AGAACTGCGG CTACCGCCGA TGCCGTGCAA GCGGCGTCCT 180

GACGACTAGC TGCGGCAACA CCCTCACCTG TTACATAAAG GCCAGGGCAG CCTGTCGAGC 240

TGCGAAGCTC CAGGATTGCT CAATGCTCGT CTGTGGCGAC GACCTTGTCG TTATCTGCGA 300

GATCGAGGGG NTCCANGAGG ATCCGTCGAN NNNNNNNNNN 340

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```
Ser Thr Val Thr Glu Ser Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
1               5                  10                  15

Cys Cys Asp Leu Asp Pro Glu Ala Arg Lys Ala Ile Arg Ser Leu Thr
            20                  25                  30

Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
        35                  40                  45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
    50                  55                  60

Gly Asn Thr Leu Thr Cys Tyr Ile Lys Ala Arg Ala Ala Cys Arg Ala
65                  70                  75                  80

Ala Lys Leu Gln Asp Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val
                85                  90                  95

Val Ile Cys Glu Ile Glu Gly Xaa Xaa Glu Asp Pro Ser Xaa Xaa Xaa
            100                 105                 110

Xaa
```

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```
CGTAGACCGT GCACCATGAG CACGAATCCT AAACCTCAAA GAAAAACCAA ACGTAACATC     60

AACCGCCGCC CACAGGACGT CAAGTTCCCG GGCGGTGGCC AGATCGTCGG TGGAGTTTAC    120

CTGTTGCCGC GCAGGGGCCC TAGATTGGGT GTGCGCGCGA CTAGGAAGAC TTCCGAGCGG    180

TCGCAACCTC GTGGGAGGCG ACAGCCTATC CCCAAGGCTC GCCGATCCGA GGGCAGGTCC    240

TGGGCTCAGC CCGGGTACCC TTGGCCCCTC TATGGCAATG AGGGCATGGG TTGGGCAGGG    300

TGGCTCCTGT CCCCCCATGG CTCCCGGCCT AGTTGGGGCC CTTCAGACCC CCGGCGTAGG    360

TCGCGTAATT TGGGTAAGGT CATCGATACC CTCACATGCG GCTTCGCCGA CCTCATGGGG    420

TACATTCCGC TCGTCGGCGC CCCCCTAGGG GGCGTTGCCA GGGCCCTGGC GCAAGGCTTC    480

CGGGATCTAC CACGTCACCA ACGATTGTTC CAATGGGAGC ATTGTGTATG AGGCGGAAGG    540

CATGATCATG CATCTCCCCG GGTGCGTGCC CTGCGTTCGG GAAGGTAATA TCTCTCGTTG    600

CTGGGTACCG TTTTCCCCCA CGCTCGCAGC CAGGAATGCT AGCGTCCCCA CTCAGGCAAT    660

TCGGCGACAC GTCGACTTGC TTGTTGGGGC GGCCACACTC TGTTCTGCTA TGTATGTGGG    720

GGACCTCTGT GGGTCCGTCT TCCTCGTCGG CCAACTGTTC ACCTTCACAW CCCGCCAGNA    780

CTACACAGTG CAAGACTGCA ATTGTTCCAT CTACCCCGGC CATATAACGG G             831
```

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Ile Asn
1               5                  10                  15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
            20                  25                  30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
        35                  40                  45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
    50                  55                  60

Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly
65                  70                  75                  80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
                85                  90                  95

Leu Leu Ser Pro His Gly Ser Arg Pro Ser Trp Gly Pro Ser Asp Pro
            100                 105                 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
        115                 120                 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
    130                 135                 140

Gly Gly Val Ala Arg Ala Leu Ala Gln Gly Phe Arg Asp Leu
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```
NNNNNNNGTC ACTGAGAGTG ATATCCGTGT CGAGGARTCA ATTTACCAAT GCTGTGACCT     60

GGCCCCCGAG GCTCGCGTAG CCATAAAGTC GCTCACTGAG CGGCTATATG TCGGGGGCCC    120

TCTCACCAAC TCAAAAGGAC AGAACTGCGG CTATCGCCGG TGCCGTGCGA GCGGTGTGCT    180

GACTACTAGC TGCGGTAACA CCCTCACATG CTACCTGAAA GCCGCCGCGG CCTGTCGAGC    240

TGCAAAGCTC CGGGAATGCA CAATGCTCGT GTGTGGCGAC GACCTCGTCG TTATCTGTGA    300

GAGTGCGGGG GTCCAGGAGG ATGCTGCAAG CCTNNNNNNN                          340
```

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```
Xaa Xaa Val Thr Glu Ser Asp Ile Arg Val Glu Xaa Ser Ile Tyr Gln
1               5                  10                  15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Val Ala Ile Lys Ser Leu Thr
            20                  25                  30

Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
        35                  40                  45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
    50                  55                  60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ala Ala Ala Cys Arg Ala
65                  70                  75                  80

Ala Lys Leu Arg Glu Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
                85                  90                  95

Val Ile Cys Glu Ser Ala Gly Val Gln Glu Asp Ala Ala Ser Xaa Xaa
            100                 105                 110

Xaa
```

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```
CTCGACAGTC ACAGAGAGAG ATATAAGNAC TGAGGAGTCC ATATACCAGG CTTGTTCCTT     60

ACCCGAGCAG GCCAGAACTG CCATACACTC ATTGACTGAG AGACTCTACG TAGGAGGGCC    120

CATGATGAAC AGCAAAGGGC AATCCTGCGG ATACAGGCAT TGCCGCGCCA GCGGAGTGCT    180

CACCACCAGT ATGGGGAATA CCATCACGTG CTACATCAAG GCCCTAGCGG CTTGTAAAGC    240

AGCAGGAATA GTGGCCCCCA CCATGCTGGT GTGCGGCGAT GACCTAGTTG TCATCTCAGA    300

GAGTCAGGGA GTCGAGGAGG ACGACCGGAA CCTGANNNNN                           340
```

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```
Ser Thr Val Thr Glu Arg Asp Ile Xaa Thr Glu Glu Ser Ile Tyr Gln
1               5                  10                  15

Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
            20                  25                  30

Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
        35                  40                  45

Cys Gly Tyr Arg His Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
```

```
    50                  55                  60

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala
65                  70                  75                  80

Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
                85                  90                  95

Val Ile Ser Glu Ser Gln Gly Val Glu Glu Asp Asp Arg Asn Leu Xaa
            100                 105                 110

Xaa
```

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

```
CTCAACCGTC ACAGAGAGGG ATATAAGAAC TGAGGAGTCC ATATACCTGG CCTGCTCCTT     60

ACCCGAGCAG GCCCGGACTG CCATACATTC ATTAACTGAG AGACTTTACG TGGGAGGGCC    120

CATGATGAAC AGCAAAGGGC AGTCCTGCGG ATACAGGCGT TGCCGCGCTA GCGGAGTGCT    180

CACCACCAGT ATGGGGAACA CCATCACGTG TTATGTGAAA GCCCTCGCAG CTTGTAAAGC    240

TGCGGGCATT GTTGCCCCCA CGATGCTGGT GTGCGGCGAT GACCTGGTTG TCATCTCAGA    300

GAGTCAGGGG GCTGAGGAGG ACGAGCGAAA CCTGAGAGTC                           340
```

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
1               5                   10                  15

Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
            20                  25                  30

Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
        35                  40                  45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
    50                  55                  60

Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys Lys Ala
65                  70                  75                  80

Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
                85                  90                  95

Val Ile Ser Glu Ser Gln Gly Ala Glu Glu Asp Glu Arg Asn Leu Arg
            100                 105                 110

Val
```

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CTCAACAGTC GCGGAGAGAG ACATCAGGAC CGAGGAGTCC ATTTACCTTG CCTGCTCCTT 60

ACCCGAGCAA GCCCGAACTG CCATACATTC ATTGACTGAG AGACTTTACG TAGGAGGGCC 120

CATGATGAAC AGCAAGGGAC AGTCCTGCGG TTACAGACGT TGCCGCGCCA GCGGAGTGCT 180

CACCACCAGC ATGGGGAATA CCATCACATG CTATGTGAAG GCATTAGCTG CCTGCAAAGC 240

TGCAGGCATC GTTGCTCCCA CGATGCTGGT TTGTGGCGAC GATCTGGTCA TCATCTCAGA 300

GAGTCAGGGA ACCGAGGAGG ATGAGCGGAA CCTGAGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Ser Thr Val Ala Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
1 5 10 15

Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
50 55 60

Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys Lys Ala
65 70 75 80

Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Ile Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg
100 105 110

Val

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```
CGNACANCCT CCAGGCCCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG      60

TACACCGGAA TTGCCGGGAA GACTGGGTCC TTTCTTGGAT AAACCCACTC TATGCCCGGC     120

CATTTGGGCG TGCCCCCGCA AGACTGCTAR CCGAGTAGCG TTGGGTTGCG AAAGGCCTTG     180

TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCGGGAGG TCTCGTAGAC CGTGCATCAT     240

GAGCACAAAT CCTAAACCTC AAAGAAAAAC CAAAAGAAAC ACTAACCGCC GCCCACAGGA     300

CGTTAAGTTC CCGGGCGGTG GCCAGATCGT TGGCGGAGTA TACTTGTTGC CNTGCAGGGG     360

NCCCAGGTNG NGTNTATGCG CAACGANGAA GACTNCCGAA CAGTCCCAGC CACGTGGGAG     420

GCGCCAGCCC ATCCCGAAAG ATCGGNGCAC CACTGGCAAG TCCTGGGGAC GTCCAGGATA     480

TCCCTGGCCC CTGTATGGGA ACGAGGGCCT CGGGTGGGCA GGGTGGCTCC TGTCCCCCCG     540

GGGCTCCCGC CCGTCATGGG GCCCCACGGA CCCCCGGCAT AGGTCGCGCA ACTTGGGTAA     600

GGTCATCGAT ACCCTCACGT NCGGCTTTNC CGACCTCATG GGGTACATTC CCGTCGTTGG     660

CGCCCCAGTA GGNGGCGTCG CCAGAGCTCT CGCGCATGGC GTGAGAGTCC TGGAGGACGG     720

GATAAACTAT GAAACAGGGA ACCTCCCCGG TTGCTCTTTC TCTATCTCCC TCCTTGCTCT     780

TCTGTCCTGA ATTACCGNGC CAGTTTCTGC TGTGGAAATC AAAAACACCA GMAACACATA     840

CATGGTGACT AACGACTGTT CAAACAGYAG CATCACCTGG CAGCTTNNGN NCGCGGTGCT     900

TCACGTTCCT GGATGCGTCC CCTGTGAACG AGAGGGCAAC AGTTCCCGGT GCTGGATTCC     960

AGTCACGCCC RACGTAKNCG TGAGCCGACC TGGTGCCCTA ACCGAGGGTT TGCGATCGCA    1020

CATCGACACC ATCGTAGCGT CCGCAACATT TTGTTCTGCC CTCTACATAG GGGATGTATG    1080

TGGCGCGATA ATGATAGCTG CCCAAGTGGT CATCGTCTCG CCGGAGCATC ATCACTTTGT    1140

CCAGGACTGT AACTGTTCCA TCTACCCGGG CCACATAACG GGGCCTCGTA TGTNG         1195
```

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1               5                   10                  15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
            20                  25                  30

Gly Val Tyr Leu Leu Xaa Cys Arg Xaa Pro Arg Xaa Xaa Xaa Cys Ala
        35                  40                  45

Thr Xaa Lys Thr Xaa Glu Gln Ser Gln Pro Arg Gly Arg Arg Gln Pro
    50                  55                  60

Ile Pro Lys Asp Arg Xaa Thr Thr Gly Lys Ser Trp Gly Arg Pro Gly
65                  70                  75                  80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
                85                  90                  95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
            100                 105                 110

Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Xaa
        115                 120                 125

Gly Phe Xaa Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
    130                 135                 140
```

Xaa Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145 150 155 160

Gly Ile Asn Tyr Glu Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165 170 175

Ser Leu Leu Ala Leu Leu Ser Ile Thr Xaa Pro Val Ser Ala Val Glu
180 185 190

Ile Lys Asn Thr Xaa Asn Thr Tyr Met Val Thr Asn Asp Cys Ser Asn
195 200 205

Xaa Ser Ile Thr Trp Gln Leu Xaa Xaa Ala Val Leu His Val Pro Gly
210 215 220

Cys Val Pro Cys Glu Arg Glu Gly Asn Ser Ser Arg Cys Trp Ile Pro
225 230 235 240

Val Thr Pro Xaa Val Xaa Val Ser Arg Pro Gly Ala Leu Thr Glu Gly
245 250 255

Leu Arg Ser His Ile Asp Thr Ile Val Ala Ser Ala Thr Phe Cys Ser
260 265 270

Ala Leu Tyr Ile Gly Asp Val Cys Gly Ala Ile Met Ile Ala Ala Gln
275 280 285

Val Val Ile Val Ser Pro Glu His His His Phe Val Gln Asp Cys Asn
290 295 300

Cys Ser Ile Tyr Pro Gly His Ile Thr Gly Pro Arg Met Xaa
305 310 315

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

ATCCACAGTC ACTGAAAGAG ACATCAGAGT TGAAGAGTCC GTTTATCTGT CCTGTTCACT 60

TCCCGAGGAG GCCCGAGCTG CCATACACTC ACTAACTGAG AGGCTGTACG TGGGAGGTCC 120

CATGCAGAAC AGCAAGGGGC AATCCTGCGG ATACAGGCGC TGCCGCGCCA GCGGGGTGCT 180

CACCACTAGC ATGGGGAATA CTCTCACATG CTACTTGAAG GCCCAGGCGG CCTGCAGGGC 240

CGCGGGCATT GTTGCACCCA CAATGCTGGT GTGTGGCGAC GACCTGGTCG TCATCTCAGA 300

GAGTCAGGGG ACTGAGAGGG ACGAGAACAA CCTGAGACCT 340

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Ser Val Tyr Leu
1 5 10 15

Ser Cys Ser Leu Pro Glu Glu Ala Arg Ala Ala Ile His Ser Leu Thr
20 25 30

```
Glu Arg Leu Tyr Val Gly Gly Pro Met Gln Asn Ser Lys Gly Gln Ser
        35                  40                  45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
    50                  55                  60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65                  70                  75                  80

Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
                85                  90                  95

Val Ile Ser Glu Ser Gln Gly Thr Glu Arg Asp Glu Asn Asn Leu Arg
            100                 105                 110

Pro
```

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```
CTCAACAGTC ACGGAGAGGG ACATCAGGAA TGAGGAGTCC ATATTCCTGG CCTGCTCGTT     60

GCCCGAGGAG GCCCGGACTG TCATACATTC GCTCACTGAG AGACTCTACA TAGGCGGGCC    120

GATGATGAAC AGCAAAGGCC AGTCCTGTGG ATACAGGCGT TGTCGCGCCA GCGGGGTGTT    180

CACCACTAGC ATGGGCAATA CCATCACGTG CTATGTGAAA GCCATGGCAG CTTGCAGAGC    240

TGCCGGGATT GACGCCCCCA CAATGTTGGT ATGTGGCGAC GACCTGGTGG TCATCTCAGA    300

GAGTCAGGGG ACCGAGGAGG ACGAGCGAAA TCTGAGAGTC                           340
```

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```
Ser Thr Val Thr Glu Arg Asp Ile Arg Asn Glu Glu Ser Ile Phe Leu
1               5                   10                  15

Ala Cys Ser Leu Pro Glu Glu Ala Arg Thr Val Ile His Ser Leu Thr
            20                  25                  30

Glu Arg Leu Tyr Ile Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
        35                  40                  45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
    50                  55                  60

Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Met Ala Ala Cys Arg Ala
65                  70                  75                  80

Ala Gly Ile Asp Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
                85                  90                  95

Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg
            100                 105                 110
```

Val

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CTCTTGACTC TACTGTCACT GAACAGGATA TCAGGGTAGA AGAAGAAATA TACCAATGTT 60

GTGACCTTGA GCCGGAGGCT AGACGGGCAA TCAAATCGCT CACGGAACGG CTTTACGTTG 120

GAGGTCCCAT GTTCAACAGC AAGGGGCTCA AATGCGGATA TCGCCGTTGC CGTGCTAGCG 180

GTGTATTGCC CACTAGCTAC GGTAATACAA TCACCTGCTA CATCAAGGCC AGAGCGGCTG 240

CTCGAGCTGC GGGCCTTCAA GACCCATCAT TCCTTGTCTG CGGAGATGAT TTGGTGGTAG 300

TGGCTGAGAG TTGCGKCGTT GATGAGGAGG ATAGGGCAGC 340

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Leu Lys
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Tyr
50 55 60

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Arg Ala Ala Ala Arg Ala
65 70 75 80

Ala Gly Leu Gln Asp Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Val Ala Glu Ser Cys Xaa Val Asp Glu Glu Asp Arg Ala Ala Leu
100 105 110

Arg

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CTCCACTGTA ACCGAAAAGG ACATCAGGCC CGAGGAAGAG GTCTATCAGT GTTGTGACCT 60

GGAGCCCGAA GCTCGCAAGG TTATTACCGC CCTCACAGAA AGACTCTACG TGGGCGGCCC 120

CATGCACAAC AGCAAGGGAG ACCTTTGTGG GTATCGGAGA TGCCGCGCAA GCGGCGTCTA 180

CACGACCAGC TTCGGAAACA CACTGACGTG CTACCTCAAA GCCTCAGCTG CTATTAGAGC 240

GGCAGGGCTG AGAGACTGCA CCATGCTGGT TTGCGGTGAC GACTTGGTCG TCATCGCTGA 300

GAGCGATGGC GTAGAGGAGG ATAACCGAGC CCTCCNAGCC 340

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Ser Thr Val Thr Glu Lys Asp Ile Arg Pro Glu Glu Glu Val Tyr Gln
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
65 70 75 80

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Asn Arg Ala Leu Xaa
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

CTCCACGGTG ACTGAAAAGG ACATCAGGGT CGAGGAAGAG ATCTATCAAT GTTGTGACCT 60

GGARCCCGAA GCCCGCAAAG CAATATCCGC CCTCACAGAG AGRCTCTACT TGGGCGGCCC 120

CATGTATAAC AGCAAAGGGG AGCTCTGCGG GTATCGGAGG TGCCGCGCGA GCGGAGTGTA 180

CACCACAAGT TTCGGGAACA CAGTGACCTG CTATCTTAAG GCCACCGCAG CTACCAGGGC 240

TGCAGGCCTA AAAGACTGCA CCATGCTGGT CTGCGGTGAC GACTTGGTCG TCATCGCCGA 300

GAGCGAGGGC GTAGAGGAGG ATTCCCAACC CCTCCGAGCC 340

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
1               5                   10                  15

Cys Cys Asp Leu Xaa Pro Glu Ala Arg Lys Ala Ile Ser Ala Leu Thr
            20                  25                  30

Glu Xaa Leu Tyr Leu Gly Gly Pro Met Tyr Asn Ser Lys Gly Glu Leu
        35                  40                  45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
    50                  55                  60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala
65                  70                  75                  80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
                85                  90                  95

Val Ile Ala Glu Ser Glu Gly Val Glu Glu Asp Ser Gln Pro Leu Arg
            100                 105                 110

Ala
```

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```
CTCCACCGTA ACCGAAAGGG ACATCAGGGT CGAGGAGGAG GTCTATCAGT GTTGTGATCT    60

GGAGCCAGAG GCCCGCAAGG CAATATCCGC CCTCACGGAG AGACTCTATG TGGGCGGTCC   120

CATGTTTAAC AGCAAGGGAG ACCTATGTGG CTACCGCAGG TGCCGCGCAA GCGGCGTCTA   180

CACCACCAGC TTCGGAAACA CACTGACCTG CTACCTCAAG GCCACGGCCG CTACCAGAGC   240

GGCCGGCCTG AAGGATTGCA CAATGCTGGT TTGCGGGGAC GACCTGGTCG TCATCGCAGA   300

GAGCGATGGC GTGGACGAGG ACCGCCGAGC CCTCCAAGCT                         340
```

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
```

```
1               5                   10                  15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Ser Ala Leu Thr
            20                  25                  30

Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Asp Leu
        35                  40                  45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
    50                  55                  60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala
65                  70                  75                  80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
                85                  90                  95

Val Ile Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Arg Ala Leu Gln
            100                 105                 110

Ala
```

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```
CTCAACAGTC ACAGAGCGCG ATGTCCAGAC GGAGCATGAC ATCTACCAGT GCTGTAAGTT     60

GGAGCCCGCA GCACGGACAG CCATCACATC GCTTACTGAC CGATTGTACT NCGGTGGTCC    120

CATGTNTAAC TCTAAAGGTC AGGCATGTGG ATACCGTAGG TGCAGGGCCA GTGGCGTCTT    180

GACCACCATC CTGGCCAATA CTCTGACTTG CTACTTGAAA GCTCAGGCGG CATGCAGAGC    240

TGCCGGGCTG AAGGACTTTG ACATGTTGGT CTGCGGAGAC GACCTTGTCG TTATTTCGGA    300

GAGTTTGGGG GTCTCGGAGG ACACTAGTGC ACTGCGAGCT                           340
```

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```
Ser Thr Val Thr Glu Arg Asp Val Gln Thr Glu His Asp Ile Tyr Gln
1               5                   10                  15

Cys Cys Lys Leu Glu Pro Ala Ala Arg Thr Ala Ile Thr Ser Leu Thr
            20                  25                  30

Asp Arg Leu Tyr Xaa Gly Gly Pro Met Xaa Asn Ser Lys Gly Gln Ala
        35                  40                  45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ile Leu
    50                  55                  60

Ala Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65                  70                  75                  80

Ala Gly Leu Lys Asp Phe Asp Met Leu Val Cys Gly Asp Asp Leu Val
```

```
                85                  90                  95

Val Ile Ser Glu Ser Leu Gly Val Ser Glu Asp Thr Ser Ala Leu Arg
            100                 105                 110

Ala
```

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```
CTCGACAGTC ACCGAGCGCG ACATCCRCAC CGAGCACGAC ATCTACCAAT GCTGCCAACT     60

TGACCCGGTG GCACGCAAGG CTATTACATC TCTGACTGAG CGGCTGTACT GCGGWGGGCC    120

CATGATGAAC TCCCGTGGTC AATCATGTGG ATACCGTAGG TGCCGAGCCA GTGGCGTGCT    180

CACCACGAGC TTGGGCAATA CCCTAACATG CTATTTGAAA GCACAAGCAG CGTGTAGGGC    240

AGCAAAGCTC AAAAACTATG ACATGTTAGT CTGCGGAGAC GATCTAGTCG TTATCGCGGA    300

GAGTGGAGGA GTCTCTGAGG ATGTTGACGC CCTGCGAGCA                           340
```

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```
Ser Thr Val Thr Glu Arg Asp Ile Xaa Thr Glu His Asp Ile Tyr Gln
1               5                   10                  15

Cys Cys Gln Leu Asp Pro Val Ala Arg Lys Ala Ile Thr Ser Leu Thr
            20                  25                  30

Glu Arg Leu Tyr Cys Xaa Gly Pro Met Met Asn Ser Arg Gly Gln Ser
        35                  40                  45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Leu
    50                  55                  60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65                  70                  75                  80

Ala Lys Leu Lys Asn Tyr Asp Met Leu Val Cys Gly Asp Asp Leu Val
                85                  90                  95

Val Ile Ala Glu Ser Gly Gly Val Ser Glu Asp Val Asp Ala Leu Arg
            100                 105                 110

Ala
```

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CTCCTCCGTC ACGGAGCGTG ACATCCGCAC TGAACACGAC ATCTATCAGT GCTGCCAATT 60

AGATCCGGTA GCACGGAAAG CCATTACATC TCTTACTGAG CGGCTGTACT GCGGCGGCCC 120

CATGTACAAC TCTCGAGGTC AGTCATGTGG GTACCGCAGG TGCCGGGCTA GTGGTGTCTT 180

CACCACAAGC TTGGGCAACA CCATGACATG CTACCTGAAG GCTCAGGCGG CTTGTAGGGC 240

AGCRAAGCTC AAAAACTTTG ACATGTTGGT CTGCGGAGAC GACCTAGTCG TTATTGCTGA 300

GAGCGGAGGA GTCCCTGAGG ATGCCGGGGC CCTGCGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Ser Ser Val Thr Glu Arg Asp Ile Arg Thr Glu His Asp Ile Tyr Gln
1 5 10 15

Cys Cys Gln Leu Asp Pro Val Ala Arg Lys Ala Ile Thr Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Arg Gly Gln Ser
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
50 55 60

Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65 70 75 80

Xaa Lys Leu Lys Asn Phe Asp Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Gly Gly Val Pro Glu Asp Ala Gly Ala Leu Arg
100 105 110

Val

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

ATCCACAGTC ACGGGGCGCG ACATACGCAC AGAACNAGAC ATTTACCTGT CCTGCCAGCT 60

CGACCCAGAG GCCCGGAAAG CCATAAAGTC TCTCACTGAG AGGCTCTATG TCGGGGGCCC 120

TATGTACAAC TCAAAGGGCC AACTCTGTGG TCAACGCCGA TGCCGAGCAA GCGGAGTACT 180

CCCCACAAGC ATGGGTAACA CCATCACATG CTTCCTGAAG GCAACCGCCG CTTGCCGAGC 240

AGCCGGCTTT ACAGATTATG ACATGTTGGT CTGCGGAGAC GATTTGGTTG TCGTAACTGA 300

GAGTGCTGGA GTCAACGAGG ATATCGCTAA CCTGCGAGCC 340

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Ser Thr Val Thr Gly Arg Asp Ile Arg Thr Glu Xaa Asp Ile Tyr Leu
1 5 10 15

Ser Cys Gln Leu Asp Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Leu
35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Met
50 55 60

Gly Asn Thr Ile Thr Cys Phe Leu Lys Ala Thr Ala Ala Cys Arg Ala
65 70 75 80

Ala Gly Phe Thr Asp Tyr Asp Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Val Thr Glu Ser Ala Gly Val Asn Glu Asp Ile Ala Asn Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CTCCACTGTC ACTGAGCAGG ACATCAGGGT AGAACTTTCC ATCTTTCAGG CCTGTGACCT 60

CAAGGACGAG GCTAGGAGGG TGATAACTTC ACTCACGGAG CGGCTTTACT GTGGTGGTCC 120

TATGTTCAAC AGCAAGGGAC AACACTGCGG TTACCGCCGC TGCCGTGCTA GTGGGGTGCT 180

ACCCACCAGC TTCGGGAACA CAATCACCTG TTACATCAAA GCAAAGGCAG CTACCAAAGC 240

TGCCGGAATT AAAAATCCAT CATTCCTTGT CTGCGGAGAT GACTTGGTCG TGATTGCTGA 300

GAGTGCAGGG ATCGATGAGG ACAAGAGCGC CTTGAGAGCT 340

(2) INFORMATICN FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Leu Ser Ile Phe Gln
1 5 10 15

Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe
50 55 60

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala
65 70 75 80

Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Lys Ser Ala Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CTCTACCGTC ACAGAGAGGG ACATACGGAC AGAAGAATCC ATCTATCTGT CTTGTCAATT 60

GCCTGAAGAG GCCCGGAAAG CCATTAAATC GCTGACAGAG AGACTATACG TGGGCGGCCC 120

GATGGAAAAC AGCAAGGGCC AGGCTTGCGG ATATAGGCGT TGCCGCGCAA GCGGGGTATT 180

CACCACAAGC TTGGGGAACA CCATGACTTG TTACATCAAA GCTAAAGCGG CTTGTAAAGC 240

CGCTGGCATT GTAGACCCGG TGATGCTCGT GTGCGGTGAC GACCTAGTGG TCATCTCAGA 300

AAGCAAGGGG GTGGAGGAGG ACCAGCGGGA CCTACGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
1 5 10 15

Ser Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
50 55 60

```
Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Lys Ala Ala Cys Lys Ala
65                  70                  75                  80

Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
                85                  90                  95

Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Arg
            100                 105                 110

Val
```

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```
CTCCACTGTC ACTGAGAGAG ACATACGGAC AGAAGAATCC ATCTAYYTGG CTTGTCAATT     60

GCCCGAAGAG GCCCGGAAGG CCATTAAATC ACTGACAGAG AGACTATACG TGGGCGGCCC    120

GATGGAAAAC AGCAAAGGCC AGGCCTGCGG ATATAGGCGT TGCCGCGCAA GCGGGGTATT    180

CACCACAAGC TTGGGGAACA CCATGACTTG TTACATCAAG GCCAARGCAG CTTGTAAAGC    240

YGCTGGCATT GTTGACCCGG TGATGCTCGT GTGCGGCGAC GACCTAGTGG TCATCTCAGA    300

GAGCAAGGGG GTAGAGGAGG ACCAGCGAGA CCTAC                               335
```

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Xaa Xaa
1               5                   10                  15

Ala Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
            20                  25                  30

Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala
        35                  40                  45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
    50                  55                  60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Xaa Ala Ala Cys Lys Xaa
65                  70                  75                  80

Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
                85                  90                  95

Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Xaa
            100                 105                 110

Xaa
```

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CGTACAGCCT CCAGGACCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG 60

TACACCGGAA TTGCCGGGAA GACTGGGTCC TTTCTTGGAT TAACCCACTC TATGCCCGGA 120

GATTTGGGCG TGCCCCCGCA AGACTGCTAG CCGAGTAGCG TTGGGTTGCG AAAGGCCTTG 180

TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCGGGAGG TCTCGTAGAC CGTGCACCAT 240

GAGCACGAAT CCTAAACCTC AAAGACAAAC CAAAAGAAAC ACCAACCGCC GCCCACAGGA 300

CGTTAAGTTC CCGGGCGGTG GCCAGATCGT TGGCGGGGTG TACTTGTTGC CGCGCAGGGG 360

CCCCAGAGTG GGTGTGCGCG CGACGAGAAA GACCTCGGAG CGGTCCCAGC CGCGTGGGAG 420

GCGCCAACCT ATCCCCAAGG TTAGGCGCAC CACCGGCCGT T 461

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Met Ser Thr Asn Pro Lys Pro Gln Arg Gln Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Val Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Val Arg Arg Thr Thr Gly Arg
65 70

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CTCTACTGTC ACAGAGAGGG ATATACGAAC AGAGGAATCC ATYTATCTGG CTTGTCAATT 60

GCCCGAAGAG GCCCGGAAGG CCATCAAATC ACTGACAGAG AGACTATACG TGGGCGGCCC 120

GATGGAAAAC AGCAAGGGCC AGGCCTGCGG ATACAGGCGT TGCCGCGCAA GCGGGGTATT 180

CACCACAAGC TTGGGGAACA CCATGACTTG TTACATCAAA GCCAAGGCGG CTTGTAAAGC 240

CGCTGGCATT GTTGACCCAG TGATGCTCGT GTGCGGCGAC GACCTAGTGG TCATCTCAGA 300

AAGCAAGGGG GTGGAGGAGG ACCAACGAGA CCTACGANTC 340

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Xaa Tyr Leu
1 5 10 15

Ala Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Lys Ala Ala Cys Lys Ala
65 70 75 80

Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Arg
100 105 110

Xaa

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ala Arg Gln Ser Asp Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

Glu Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln
1   5   10

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

Ala Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln
1   5   10

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Asp Arg Arg Thr Thr Gly Lys Ser Trp Gly Arg
1   5   10

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Asp Arg Arg Ala Thr Gly Arg Ser Trp Gly Arg
1   5   10

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Asp Arg Arg Ala Thr Gly Lys Ser Trp Gly Arg
1   5   10

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Val Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln
1   5   10

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Val Arg His Gln Thr Gly Arg Thr Trp Ala Gln
1   5   10

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Arg Gln Asn Gln Gly Arg Thr Trp Ala Gln
1   5   10

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln
1   5   10

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

Val Arg Arg Thr Thr Gly Arg Xaa Xaa Xaa Xaa
1   5   10

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Val Arg Arg Thr Thr Gly Arg Thr Trp Ala Gln
1   5   10

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Tyr Glu Val His Ser Thr Thr Asp Gly Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Val Glu Val Lys Asn Thr Ser Gln Ala Tyr Met Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Ile Gln Val Lys Asn Asn Ser His Phe Tyr Met Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```
Val Gln Val Lys Asn Thr Ser Thr Met Tyr Met Ala
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```
Val Gln Val Lys Asn Thr Ser His Ser Tyr Met Val
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```
Val Gln Val Ala Asn Arg Ser Gly Ser Tyr Met Val
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```
Val Glu Ile Lys Asn Thr Xaa Asn Thr Tyr Val Leu
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```
Val Glu Ile Lys Asn Thr Ser Asn Thr Tyr Val Leu
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Ile Asn Tyr Arg Asn Val Ser Gly Ile Tyr Tyr Val
1   5   10

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Ile Asn Tyr Arg Asn Thr Ser Gly Ile Tyr His Val
1   5   10

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Ile Asn Tyr His Asn Thr Ser Gly Ile Tyr His Ile
1   5   10

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val
1   5   10

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val
1   5   10

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

Ile Gln Val Lys Asn Ala Ser Gly Ile Tyr His Leu

1   5   10

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Ala His Tyr Thr Asn Lys Ser Gly Leu Tyr His Leu
1   5   10

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Leu Asn Tyr Ala Asn Lys Ser Gly Leu Tyr His Leu
1   5   10

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Leu Glu Tyr Arg Asn Ala Ser Gly Leu Tyr Met Val
1   5   10

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Ile Tyr Glu Met Asp Gly Met Ile Met His Tyr
1   5   10

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Ile Tyr Glu Met Ser Gly Met Ile Leu His Ala
1   5   10

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

Val Tyr Glu Ala Lys Asp Ile Ile Leu His Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

Val Trp Gln Leu Xaa Asp Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

Val Trp Gln Leu Arg Asp Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Ile Trp Gln Met Gln Gly Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

Val Trp Gln Leu Lys Asp Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

Val Trp Gln Leu Glu Glu Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

Thr Trp Gln Leu Xaa Xaa Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Val Tyr Glu Ala Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

Val Tyr Glu Ala Asp His His Ile Leu Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

Val Phe Glu Ala Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

Val Tyr Glu Ser Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Val Phe Glu Glu Thr Met Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Val Tyr Glu Ala Glu Thr Leu Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Val Tyr Glu Ala Asn Gly Met Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

Val Tyr Glu Ala Gly Asp Ile Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Val Arg Glu Asp Asn His Leu Arg Cys Trp Met Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Met Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Ile Arg Glu Gly Asn Ile Ser Arg Cys Trp Val Leu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

Glu Asn Ser Ser Gly Arg Phe His Cys Trp Ile Pro Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Glu Arg Ser Gly Asn Arg Thr Phe Cys Trp Thr Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

Glu Leu Gln Gly Asn Lys Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Glu Arg His Gln Asn Gln Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

Glu Trp Lys Asp Asn Thr Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Glu Arg Glu Gly Asn Ser Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Val Arg Glu Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Val Arg Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

Val Arg Val Gly Asn Gln Ser Ser Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Val Lys Glu Gly Asn His Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Val Lys Thr Gly Asn Thr Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Ile Lys Ala Gly Asn Glu Ser Arg Cys Trp Leu Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Val Lys Xaa Xaa Asn Gln Ser Arg Cys Trp Val Gln Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Val Lys Thr Gly Asn Leu Thr Lys Cys Trp Leu Ser Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Val Arg Ser Gly Asn Thr Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Val Lys Asn Ala Ser Val Pro Thr Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Val Lys Asp Ala Asn Val Pro Thr Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

Ala Arg Ile Ala Asn Ala Pro Ile Asp Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Val Ser Lys Pro Gly Ala Leu Thr Lys Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

Val Ser Arg Pro Gly Ala Leu Thr Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Val Asn Gln Pro Gly Ala Leu Thr Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Val Ser Gln Pro Gly Ala Leu Thr Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

Val Ser Arg Pro Gly Ala Leu Thr Glu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Ala Pro Tyr Ile Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Ala Pro Tyr Thr Ala Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Ala Pro Ile Leu Ser Ala Pro Leu Met Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Val Pro Asn Ser Ser Val Pro Ile His Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Val Pro Asn Ala Ser Thr Pro Val Thr Gly
1   5   10

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

Val Gln Asn Ala Ser Val Ser Ile Arg Gly
1   5   10

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Val Lys Ser Pro Cys Ala Ala Thr Ala Ser
1   5   10

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Ser Pro Arg Met His His Thr Thr Gln Glu
1   5   10

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Ser Pro Arg Leu Tyr His Thr Thr Gln Glu
1   5   10

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Thr Ser Arg Arg His Trp Thr Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Ala Pro Lys Arg His Tyr Phe Val Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Ser Pro Gln Tyr His Thr Phe Val Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Ser Pro Gln His His Asn Phe Ser Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Ser Pro Gln His His Ile Phe Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Ser Pro Glu His His His Phe Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp
1   5   10

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Arg Pro Arg Arg His Trp Thr Ala Gln Asp
1   5   10

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

Gln Pro Arg Arg His Trp Thr Thr Gln Asp
1   5   10

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Arg Pro Arg Arg His Trp Thr Thr Gln Glu
1   5   10

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

Gln Pro Arg Arg His Trp Thr Val Gln Asp
1   5   10

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Arg Pro Lys Tyr His Gln Val Thr Gln Asp
1   5   10

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

Arg Pro Arg Met His Gln Val Val Gln Glu
1   5   10

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Arg Pro Arg Met Tyr Glu Ile Ala Gln Asp
1   5   10

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

Arg His Arg Gln His Trp Thr Val Gln Asp
1   5   10